CLAIMS

Sub B3

1. A process for detecting numerical changes in cell DNA, comprising the following steps:

(a) isolating DNA from cells which have no known numerical changes in their DNA, and amplifying the DNA by means of a PCR method using tag primers;

(b) hybridizing of cells under study *in situ* with the amplified DNA from (a);

(c) amplifying DNA from the *in situ* hybridized cells from (b) by means of a PCR method using the tag primers from (a); and

(d) identifying numerical changes in the amplified DNA from (c).

2. The process according to claim 1, wherein the cells under study originate from tumors.

3. The process according to claim 1, wherein the cells under study originate from the blood of pregnant persons.

Sub B4

4. The process according to claim 1, wherein the cells under study are those of a small cell population or single cells.

5. The process according to claim 1, wherein the cells under study have a nucleus in interphase.

6. The process according to claim 1, wherein the tag primers are degenerative primers.

7 The process according to claim 1, wherein the identifying is performed by a "Comparative Genomic Hybridization" (CGH) method.

Sub B5

8. A kit for carrying out the process according to claim 1, comprising the following components:

(a) amplified DNA from cells that have no known numerical changes in their DNA, the DNA being flanked by tag primers;

Sub B5

(b) tag primers; and

(c) auxiliary agents for identifying numerical changes in a DNA.